

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/381,497A

DATE: 05/21/2001  
TIME: 11:16:56

Input Set : A:\-317-1.app  
Output Set: N:\CRF3\05212001\I381497A.raw

## SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:  
6 (i) APPLICANT: FitzGerald, David  
7 Pastan, Ira  
8 Mansfield, Elizabeth  
9 Kreitman, Robert  
11 (ii) TITLE OF INVENTION: Recombinant Antibodies and  
12 Immunoconjugates Targeted to CD-22 Bearing Cells and  
13 Tumors  
15 (iii) NUMBER OF SEQUENCES: 15  
17 (iv) CORRESPONDENCE ADDRESS:  
18 (A) ADDRESSEE: Townsend and Townsend and Crew LLP  
19 (B) STREET: Two Embarcadero Center, Eighth Floor  
20 (C) CITY: San Francisco  
21 (D) STATE: California  
22 (E) COUNTRY: USA  
23 (F) ZIP: 94111-3834  
25 (v) COMPUTER READABLE FORM:  
26 (A) MEDIUM TYPE: Floppy disk  
27 (B) COMPUTER: IBM PC compatible  
28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
31 (vi) CURRENT APPLICATION DATA:  
C--> 32 (A) APPLICATION NUMBER: US/09/381,497A  
C--> 33 (B) FILING DATE: 21-May-2001  
34 (C) CLASSIFICATION:  
40 (vii) PRIOR APPLICATION DATA:  
37 (A) APPLICATION NUMBER: WO PCT/US98/05453  
38 (B) FILING DATE: 19-MAR-1998  
41 (A) APPLICATION NUMBER: US 60/041,437  
42 (B) FILING DATE: 20-MAR-1997  
44 (viii) ATTORNEY/AGENT INFORMATION:  
45 (A) NAME: Weber, Ellen Lauver  
46 (B) REGISTRATION NUMBER: 32,762  
47 (C) REFERENCE/DOCKET NUMBER: 015280-317100US  
49 (ix) TELECOMMUNICATION INFORMATION:  
50 (A) TELEPHONE: (415) 576-0200  
51 (B) TELEFAX: (415) 576-0300  
54 (2) INFORMATION FOR SEQ ID NO: 1:  
56 (i) SEQUENCE CHARACTERISTICS:  
57 (A) LENGTH: 369 base pairs  
58 (B) TYPE: nucleic acid  
59 (C) STRANDEDNESS: single  
60 (D) TOPOLOGY: linear  
W--> 62 (ii) MOLECULE TYPE: DNA  
65 (ix) FEATURE:  
66 (A) NAME/KEY: CDS

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67          (B) LOCATION: 1..369
68          (D) OTHER INFORMATION: /product= "RFB4 heavy chain"
71          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
73 GAA GTG CAG CTG GTG GAG TCT GGG GGA GGC TTA GTG AAG CCT GGA GGG      48
74 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
75   1           5           10           15
77 TCC CTG AAA CTC TCC TGT GCA GCC TCT GGA TTC GCT TTC AGT ATC TAT      96
78 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
79           20           25           30
81 GAC ATG TCT TGG GTT CGC CAG ACT CCG GAG AAG AGG CTG GAG TGG GTC      144
82 Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
83           35           40           45
85 GCA TAC ATT AGT AGT GGT GGT GGT ACC ACC TAC TAT CCA GAC ACT GTG      192
86 Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
87           50           55           60
89 AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT GCC AAG AAC ACC CTG TAC      240
90 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
91   65           70           75           80
93 CTG CAA ATG AGC AGT CTG AAG TCT GAG GAC ACA GCC ATG TAT TAC TGT      288
94 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
95           85           90           95
97 GCA AGA CAT AGT GGC TAC GGT AGT AGC TAC GGG GTT TTG TTT GCT TAC      336
98 Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
99           100          105          110
101 TGG GGC CAA GGG ACT CTG GTC ACT GTC TCT GCA      369
102 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
103           115          120
106 (2) INFORMATION FOR SEQ ID NO: 2:
108      (i) SEQUENCE CHARACTERISTICS:
109          (A) LENGTH: 123 amino acids
110          (B) TYPE: amino acid
111          (D) TOPOLOGY: linear
113      (ii) MOLECULE TYPE: protein
115      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
117 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
118   1           5           10           15
120 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
121           20           25           30
123 Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
124           35           40           45
126 Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
127           50           55           60
129 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
130   65           70           75           80
132 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
133           85           90           95
135 Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
136           100          105          110
138 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala

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139          115          120
142 (2) INFORMATION FOR SEQ ID NO: 3:
144     (i) SEQUENCE CHARACTERISTICS:
145         (A) LENGTH: 321 base pairs
146         (B) TYPE: nucleic acid
147         (C) STRANDEDNESS: single
148         (D) TOPOLOGY: linear
W--> 150     (ii) MOLECULE TYPE: DNA
153     (ix) FEATURE:
154         (A) NAME/KEY: CDS
155         (B) LOCATION: 1..321
156         (D) OTHER INFORMATION: /product= "RFB4 light chain"
159     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
161 GAT ATC CAG ATG ACC CAG ACT ACA TCC TCC CTG TCT GCC TCT CTG GGA      48
162 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
163 1      5      10      15
165 GAC AGA GTC ACC ATT AGT TGC AGG GCA AGT CAG GAC ATT AGC AAT TAT      96
166 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
167      20      25      30
169 TTA AAC TGG TAT CAG CAG AAA CCA GAT GGA ACT GTT AAA CTC CTG ATC      144
170 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
171      35      40      45
173 TAC TAC ACA TCA ATA TTA CAC TCA GGA GTC CCA TCA AGG TTC AGT GGC      192
174 Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
175      50      55      60
177 AGT GGG TCT GGA ACA GAT TAT TCT CTC ACC ATT AGC AAC CTG GAG CAA      240
178 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
179      65      70      75      80
181 GAA GAT TTT GCC ACT TAC TTT TGC CAA CAG GGT AAT ACG CTT CCG TGG      288
182 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
183      85      90      95
185 ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA      321
186 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
187      100      105
190 (2) INFORMATION FOR SEQ ID NO: 4:
192     (i) SEQUENCE CHARACTERISTICS:
193         (A) LENGTH: 107 amino acids
194         (B) TYPE: amino acid
195         (D) TOPOLOGY: linear
197     (ii) MOLECULE TYPE: protein
199     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
201 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
202 1      5      10      15
204 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
205      20      25      30
207 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
208      35      40      45
210 Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
211      50      55      60

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213 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln  
 214 65 70 75 80  
 216 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp  
 217 85 90 95  
 219 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
 220 100 105

223 (2) INFORMATION FOR SEQ ID NO: 5:

225 (i) SEQUENCE CHARACTERISTICS:

226 (A) LENGTH: 4 amino acids

227 (B) TYPE: amino acid

228 (C) STRANDEDNESS:

229 (D) TOPOLOGY: linear

231 (ii) MOLECULE TYPE: peptide

234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

236 Gly Gly Gly Ser

237 1

240 (2) INFORMATION FOR SEQ ID NO: 6:

242 (i) SEQUENCE CHARACTERISTICS:

243 (A) LENGTH: 33 base pairs

244 (B) TYPE: nucleic acid

245 (C) STRANDEDNESS: single

246 (D) TOPOLOGY: linear

W--&gt; 248 (ii) MOLECULE TYPE: DNA

251 (ix) FEATURE:

252 (A) NAME/KEY: -

253 (B) LOCATION: 1..33

254 (D) OTHER INFORMATION: /note= "RFB4 VH5 heavy chain primer"

257 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

259 GGACCTCATA TGGAAGTGCA GCTGGTGGAG TCT

33

262 (2) INFORMATION FOR SEQ ID NO: 7:

264 (i) SEQUENCE CHARACTERISTICS:

265 (A) LENGTH: 24 base pairs

266 (B) TYPE: nucleic acid

267 (C) STRANDEDNESS: single

268 (D) TOPOLOGY: linear

W--&gt; 270 (ii) MOLECULE TYPE: DNA

273 (ix) FEATURE:

274 (A) NAME/KEY: -

275 (B) LOCATION: 1..24

276 (D) OTHER INFORMATION: /note= "gamma-CH1 heavy chain primer"

279 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

281 AGCAGATCCA GGGGCCAGTG GATA

24

284 (2) INFORMATION FOR SEQ ID NO: 8:

286 (i) SEQUENCE CHARACTERISTICS:

287 (A) LENGTH: 54 base pairs

288 (B) TYPE: nucleic acid

289 (C) STRANDEDNESS: single

290 (D) TOPOLOGY: linear

W--&gt; 292 (ii) MOLECULE TYPE: DNA

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295      (ix) FEATURE:
296          (A) NAME/KEY: -
297          (B) LOCATION: 1..54
298          (D) OTHER INFORMATION: /note= "RFB4 VH3 heavy chain primer"
301      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
303 AGATCCGCCA CCACCGGATC CGCCTCCGCC TGCAGAGACA GTGACCAGAG TCCC      54
306 (2) INFORMATION FOR SEQ ID NO: 9:
308     (i) SEQUENCE CHARACTERISTICS:
309         (A) LENGTH: 27 base pairs
310         (B) TYPE: nucleic acid
311         (C) STRANDEDNESS: single
312         (D) TOPOLOGY: linear
W--> 314     (ii) MOLECULE TYPE: DNA
317     (ix) FEATURE:
318         (A) NAME/KEY: -
319         (B) LOCATION: 1..27
320         (D) OTHER INFORMATION: /note= "RFB4 VH3 dsFv heavy chain
321 primer"
325     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
327 CCGGAAGCTT TTGCAGAGAC AGTGACC      27
330 (2) INFORMATION FOR SEQ ID NO: 10:
332     (i) SEQUENCE CHARACTERISTICS:
333         (A) LENGTH: 28 base pairs
334         (B) TYPE: nucleic acid
335         (C) STRANDEDNESS: single
336         (D) TOPOLOGY: linear
W--> 338     (ii) MOLECULE TYPE: DNA
341     (ix) FEATURE:
342         (A) NAME/KEY: -
343         (B) LOCATION: 1..28
344         (D) OTHER INFORMATION: /note= "RFB4 VH dsFv(cys) heavy chain
345 primer"
348     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
350 GACCCACTCC AGGCACTTCT CCGGAGTC      28
353 (2) INFORMATION FOR SEQ ID NO: 11:
355     (i) SEQUENCE CHARACTERISTICS:
356         (A) LENGTH: 48 base pairs
357         (B) TYPE: nucleic acid
358         (C) STRANDEDNESS: single
359         (D) TOPOLOGY: linear
W--> 361     (ii) MOLECULE TYPE: DNA
364     (ix) FEATURE:
365         (A) NAME/KEY: -
366         (B) LOCATION: 1..48
367         (D) OTHER INFORMATION: /note= "RFB4 VL5 light chain primer"
370     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
372 GGTGGCGGAT CTGGAGGTGG CGGAAGCGAT ATCCAGATGA CACAGACT      48
375 (2) INFORMATION FOR SEQ ID NO: 12:
377     (i) SEQUENCE CHARACTERISTICS:

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## VERIFICATION SUMMARY

DATE: 05/21/2001

PATENT APPLICATION: US/09/381,497A

TIME: 11:16:58

Input Set : A:\-317-1.app

Output Set: N:\CRF3\05212001\I381497A.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:62 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1  
L:150 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3  
L:248 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6  
L:270 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7  
L:292 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8  
L:314 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9  
L:338 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10  
L:361 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11  
L:383 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12  
L:405 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13  
L:427 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14  
L:450 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15